

**IN THE SPECIFICATION**

Please substitute the following paragraph 28 for that currently on record at page 16, first full paragraph:

We next evaluated the ability of Digital Karyotyping to detect subchromosomal changes, particularly gains and losses of chromosomal arms. Tag densities were analyzed along each chromosome using sliding windows containing 1000 virtual tags (~4 Mb), as windows of this size were predicted to reliably detect such alterations (Table 1). For the NLB sample, tag density maps showed uniform content along each chromosome, with small variations (<1.5 fold) present over localized regions, presumably due to overrepresentation of tags matching repeated sequences (data not shown). In contrast, the DiFi tag density map (normalized to the NLB data) revealed widespread changes, including apparent losses in large regions of 5q, 8p and 10q, and gains of 2p, 7q, 9p, 12q, 13q, and 19q (Fig. 2 and Fig. 5). These changes included regions of known tumor suppressor genes (21) and other areas commonly altered in colorectal cancer (11, 12, 22). These alterations were confirmed by chromosomal CGH analyses, which revealed aberrations that were largely consistent with Digital Karyotype analyses in both location and amplitude (Fig. 2 and Fig. 5).